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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/939,226

DATE: 11/19/2001  
 TIME: 08:52:05

Input Set : N:\Crf3\RULE60\09939226.raw  
 Output Set: N:\CRF3\11192001\I939226.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: SAMSON, MICHEL  
 6 PARMENTIER, MARC  
 7 VASSART, GILBERT  
 8 LIBERT, FREDERICK

10 (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
 11 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

13 (iii) NUMBER OF SEQUENCES: 17

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear  
 17 (B) STREET: 620 Newport Center Drive 16th Floor  
 18 (C) CITY: Newport Beach  
 19 (D) STATE: CA  
 20 (E) COUNTRY: U.S.A.  
 21 (F) ZIP: 92660

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk  
 25 (B) COMPUTER: IBM PC compatible  
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/939,226  
 C--> 31 (B) FILING DATE: 24-Aug-2001  
 32 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/626,939  
 37 (B) FILING DATE: 2000-07-27

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Altman, Daniel E  
 44 (B) REGISTRATION NUMBER: 34,115  
 45 (C) REFERENCE/DOCKET NUMBER:

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 792 base pairs  
 51 (B) TYPE: nucleic acid  
 52 (C) STRANDEDNESS: single  
 53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

58 (ix) FEATURE:

59 (A) NAME/KEY: CDS  
 60 (B) LOCATION: 240..791

63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

65 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAAGCTAG CAGCAAACCT	60
66 TCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC	120
67 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCCATG GAGGGCAACT	180
68 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG	239

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69	ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA	287
70	Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr	
71	1 5 10 15	
72	TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC	335
73	Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
74	20 25 30	
75	CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC	383
76	Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn	
77	35 40 45	
78	ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG	431
79	Met Leu Val Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
80	50 55 60	
81	ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT	479
82	Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu	
83	65 70 75 80	
84	CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT	527
85	Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Gln Trp Asp Phe	
86	85 90 95	
87	GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC	575
88	Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe	
89	100 105 110	
90	TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG	623
91	Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
92	115 120 125	
93	GCT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	671
94	Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe	
95	130 135 140	
96	GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT	719
97	Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser	
98	145 150 155 160	
99	CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC	767
100	Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr	
101	165 170 175	
102	ACC TGC AGC TCT CAT TTT CCA TAC A	792
103	Thr Cys Ser Ser His Phe Pro Tyr	
104	180	
107	(2) INFORMATION FOR SEQ ID NO: 2:	
109	(i) SEQUENCE CHARACTERISTICS:	
110	(A) LENGTH: 1477 base pairs	
111	(B) TYPE: nucleic acid	
112	(C) STRANDEDNESS: single	
113	(D) TOPOLOGY: linear	
115	(ii) MOLECULE TYPE: DNA (genomic)	
118	(ix) FEATURE:	
119	(A) NAME/KEY: CDS	
120	(B) LOCATION: 240..1295	
123	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
125	GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAAGCTAG CAGCAAACCT	60
126	TCCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC	120

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127	TATGTAGGCA	ATTAAAAACC	TATTGATGTA	TAAAACAGTT	TGCATTCATG	GAGGGCAACT	180
128	AAATACATTC	TAGGACTTTA	TAAAAGATCA	CTTTTATTT	ATGCACAGGG	TGGAACAAAG	239
129	ATG GAT TAT	CAA GTG TCA	AGT CCA ATC	TAT GAC ATC	AAT TAT TAT	ACA	287
130	Met Asp Tyr	Gln Val Ser	Ser Pro Ile	Tyr Asp Ile	Asn Tyr Tyr	Thr	
131	1	5	10	15			
132	TCG GAG CCC	TGC CAA AAA	ATC AAT GTG	AAG CAA ATC	GCA GCC CGC	CTC	335
133	Ser Glu Pro	Cys Gln Lys	Ile Asn Val	Lys Gln Ile	Ala Ala Arg	Leu	
134	20	25	30				
135	CTG CCT CCG	CTC TAC TCA	CTG GTG	TTC ATC TTT	GGT TTT GTG	GGC AAC	383
136	Leu Pro Pro	Leu Tyr Ser	Leu Val Phe	Ile Phe Gly	Phe Val Gly	Asn	
137	35	40	45				
138	ATG CTG GTC	ATC CTC ATC	CTG ATA AAC	TGC AAA AGG	CTG AAG AGC	ATG	431
139	Met Leu Val	Ile Leu Ile	Leu Asn Cys	Lys Arg Leu	Lys Ser Met		
140	50	55	60				
141	ACT GAC ATC	TAC CTG CTC	AAC CTG GCC	ATC TCT GAC	CTG TTT TTC	CTT	479
142	Thr Asp Ile	Tyr Leu Leu	Asn Leu Ala	Ile Ser Asp Leu	Phe Phe Leu		
143	65	70	75	80			
144	CTT ACT GTC	CCC TTC TGG	GCT CAC TAT	GCT GCC GCC	CAG TGG GAC	TTT	527
145	Leu Thr Val	Pro Phe Trp	Ala His Tyr	Ala Ala Gln	Trp Asp Phe		
146	85	90	95				
147	GGA AAT ACA	ATG TGT CAA	CTC TTG ACA	GGG CTC TAT	TTT ATA GGC	TTC	575
148	Gly Asn Thr	Met Cys Gln	Leu Leu Thr	Gly Leu Tyr	Phe Ile Gly	Phe	
149	100	105	110				
150	TTC TCT GGA	ATC TTC ATC	ATC CTC CTG	ACA ATC GAT	AGG TAC CTG		623
151	Phe Ser Gly	Ile Phe Phe	Ile Ile Leu	Leu Thr Ile	Asp Arg Tyr	Leu	
152	115	120	125				
153	GCT GTC GTC	CAT GCT GTG	TTT GCT TTA	AAA GCC AGG	ACG GTC ACC	TTT	671
154	Ala Val Val	His Ala Val	Phe Ala Leu	Lys Ala Arg	Thr Val Thr	Phe	
155	130	135	140				
156	GGG GTG GTG	ACA AGT GTG	ATC ACT TGG	GTG GTG GCT	GTG TTT GCG	TCT	719
157	Gly Val Val	Thr Ser Val	Ile Thr Trp	Val Val Ala	Val Phe Ala	Ser	
158	145	150	155	160			
159	CTC CCA GGA	ATC ATC TTT	ACC AGA TCT	CAA AAA GAA	GGT CTT CAT	TAC	767
160	Leu Pro Gly	Ile Ile Phe	Thr Arg Ser	Gln Lys Glu	Gly Leu His	Tyr	
161	165	170	175				
162	ACC TGC AGC	TCT CAT TTT	CCA TAC AGT	CAG TAT CAA	TTC TGG AAG	AAT	815
163	Thr Cys Ser	Ser His Phe	Pro Tyr Ser	Gln Tyr Gln	Phe Trp Lys	Asn	
164	180	185	190				
165	TTC CAG ACA	TTA AAG ATA	GTC ATC TTG	GGG CTG GTC	CTG CCG CTG	CTT	863
166	Phe Gln Thr	Leu Lys Ile	Val Ile Leu	Gly Leu Val	Leu Pro Leu	Leu	
167	195	200	205				
168	GTC ATG GTC	ATC TGC TAC	TCG GGA ATC	CTA AAA ACT	CTG CTT CGG	TGT	911
169	Val Met Val	Ile Cys Tyr	Ser Gly Ile	Leu Lys Thr	Leu Leu Arg	Cys	
170	210	215	220				
171	CGA AAT GAG	AAG AAG AGG	CAC AGG GCT	GTG AGG CTT	ATC TTC ACC	ATC	959
172	Arg Asn Glu	Lys Lys Arg	His Arg Ala	Val Arg Leu	Ile Phe Thr	Ile	
173	225	230	235	240			
174	ATG ATT GTT	TAT TTT CTC	TTC TGG GCT	CCC TAC AAC ATT	GTC CTT CTC		1007
175	Met Ile Val	Tyr Phe Leu	Phe Trp Ala	Pro Tyr Asn	Ile Val Leu	Leu	

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176	245	250	255	
177 CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT				1055
178 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser				
179 260	265	270		
180 AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG				1103
181 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr				
182 275	280	285		
183 CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC				1151
184 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe				
185 290	295	300		
186 AGA AAC TAC CTC TTA GTC TTC CAA AAG CAC ATT GCC AAA CGC TTC				1199
187 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe				
188 305	310	315	320	
189 TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC				1247
190 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser				
191 325	330	335		
192 TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG				1295
193 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu				
194 340	345	350		
195 TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTCA				1355
196 TACACAGCCT GGGCTGGGG TNGGTTGGNN GAGGTCTTTT TTAAAAGGAA GTTACTGTTA				1415
197 TAGAGGGTCT AAGATTTCATC CATTATTG GCATCTGTT AAAGTAGATT AGATCCGAAT				1475
198 TC				1477
201 (2) INFORMATION FOR SEQ ID NO: 3:				
203 (i) SEQUENCE CHARACTERISTICS:				
204 (A) LENGTH: 1442 base pairs				
205 (B) TYPE: nucleic acid				
206 (C) STRANDEDNESS: single				
207 (D) TOPOLOGY: linear				
209 (ii) MOLECULE TYPE: DNA (genomic)				
212 (ix) FEATURE:				
213 (A) NAME/KEY: CDS				
214 (B) LOCATION: 240..884				
217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:				
219 GAATTCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAGCTAG CAGCAAACCT				60
220 TCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC				120
221 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCATG GAGGGCAACT				180
222 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTG ATGCACAGGG TGGAACAAAG				239
223 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA				287
224 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr				
225 1 5 10 15				
226 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC				335
227 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu				
228 20 25 30				
229 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC				383
230 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn				
231 35 40 45				
232 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG				431
233 Met Leu Val Ile Leu Ile Leu Asn Cys Lys Arg Leu Lys Ser Met				

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234	50	55	60	
235	ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT			479
236	Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu			
237	65	70	75	80
238	CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT			527
239	Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe			
240	85	90	95	
241	GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC			575
242	Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe			
243	100	105	110	
244	TTC TCT GGA ATC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG			623
245	Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu			
246	115	120	125	
247	GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT			671
248	Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe			
249	130	135	140	
250	GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT			719
251	Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser			
252	145	150	155	160
253	CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC			767
254	Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr			
255	165	170	175	
256	ACC TGC AGC TCT CAT TTT CCA TAC ATT AAA GAT AGT CAT CTT GGG GCT			815
257	Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala			
258	180	185	190	
259	GGT CCT GCC GCT GCT TGT CAT GGT CAT CTG CTA CTC GGG AAT CCT AAA			863
260	Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys			
261	195	200	205	
262	AAC TCT GCT TCG GTG TCG AAA TGAGAAGAAG AGGCACAGGG CTGTGAGGCT			914
263	Asn Ser Ala Ser Val Ser Lys			
264	210	215		
265	TATCTCACCC ATCATGATTG TTTATTTCT CTTCTGGGCT CCCTACAACA TTGTCCTTCT			974
266	CCTGAACACC TTCCAGGAAT TCTTTGGCCT GAATAATTGC AGTAGCTCTA ACAGGTTGGA			1034
267	CCAAGCTATG CAGGTGACAG AGACTCTTGG GATGACGCAC TGCTGCATCA ACCCCATCAT			1094
268	CTATGCCTTT GTCGGGGAGA AGTTTCAGAAA CTACCTCTTA GTCTTCTTCC AAAAGCACAT			1154
269	TGCCAACCGC TTCTGCAAAT GCTGTTCTAT TTTCCAGCAA GAGGCTCCCG AGCGAGCAAG			1214
270	CTCAGTTTAC ACCCGATCCA CTGGGGAGCA GGAAATATCT GTGGGCTGT GACACGGACT			1274
271	CAAGTGGGCT GGTGACCCAG TCAGAGTTGT GCACATGGCT TAGTTTCAT ACACAGCCTG			1334
272	GGCTGGGGGT GGTTGGGAGG TCTTTTTAA AAGGAAGTTA CTGTTATAGA GGGTCTAAGA			1394
273	TTCATCCATT TATTTGGCAT CTGTTAAAG TAGATTAGAT CCGAATTTC			1442
276	(2) INFORMATION FOR SEQ ID NO: 4:			
278	(i) SEQUENCE CHARACTERISTICS:			
279	(A) LENGTH: 184 amino acids			
280	(B) TYPE: amino acid			
281	(D) TOPOLOGY: linear			
283	(ii) MOLECULE TYPE: protein			
285	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:			
287	Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr			
288	1	5	10	15

VERIFICATION SUMMARY  
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Input Set : N:\Crf3\RULE60\09939226.raw  
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:418 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:536 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10